



SEQUENCE LISTING

<110> Cohen, Stanley N.
Li, Limin

<120> MAMMALIAN TUMOR SUSCEPTIBILITY GENES AND THEIR USES

<130> 70017.27USC2

<140> US 10/697,720

<141> 2003-10-29

<150> US 09/804,690

<151> 2001-03-12

<150> US 09/146,187

<151> 1998-09-01

<150> US 08/977,818

<151> 1997-11-25

<150> US 08/670,274

<151> 1996-06-13

<150> US 08/585,758

<151> 1996-01-16

<150> US 60/006,856

<151> 1995-11-16

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 1448

<212> DNA

<213> Artificial Sequence

<220>

<223> TSG101 nucleotide

<220>

<221> CDS

<222> (61)..(1203)

<400> 1

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atg atg tcc aag tac aaa tat aga gat cta acc gtc cgt caa act gtc 108
Met Met Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Gln Thr Val
1 5 10 15

aat gtc atc gct atg tac aaa gat ctc aaa cct gta ttg gat tca tat 156
Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
20 25 30

gtt ttt aat gat ggc agt tcc agg gag ctg gtg aac ctc act ggt aca 204
Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr

35	40	45	
atc cca gtg cgt tat cga ggt aat ata tat aat att cca ata tgc ctg Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu 50 55 60			252
tgg ctg ctg gac aca tac cca tat aac ccc cct atc tgt ttt gtt aag Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys 65 70 75 80			300
cct act agt tca atg act att aaa aca gga aag cat gtg gat gca aat Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn 85 90 95			348
ggg aaa atc tac cta cct tat cta cat gac tgg aaa cat cca cgg tca Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser 100 105 110			396
gag ttg ctg gag ctt att caa atc atg att gtg ata ttt gga gag gag Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu 115 120 125			444
cct cca gtg ttc tcc cgg cct act gtt tct gca tcc tac cca cca tac Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr 130 135 140			492
aca gca aca ggg cca cca aat acc tcc tac atg cca ggc atg cca agt Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser 145 150 155 160			540
gga atc tct gca tat cca tct gga tac cct ccc aac ccc agt ggt tat Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr 165 170 175			588
cct ggc tgt cct tac cca cct gct ggc cca tac cct gcc aca aca agc Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser 180 185 190			636
tca cag tac cct tcc cag cct cct gtg acc act gtt ggt ccc agc aga Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg 195 200 205			684
gat ggc aca atc agt gag gac act atc cgt gca tct ctc atc tca gca Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala 210 215 220			732
gtc agt gac aaa ctg aga tgg cgg atg aag gag gaa atg gat ggt gcc Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala 225 230 235 240			780
cag gca gag ctt aat gcc ttg aaa cga aca gag gaa gat ctg aaa aaa Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys 245 250 255			828
ggc cac cag aaa ctg gaa gag atg gtc acc cgc tta gat caa gaa gta Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val 260 265 270			876
gct gaa gtt gat aaa aac ata gaa ctt ttg aaa aag aag gat gaa gaa Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu 280 285 290 295 300			924

275	280	285	
cta agt tct gct ctg gag aaa atg gaa aat caa tct gaa aat aat gat			972
Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp			
290	295	300	
att gat gaa gtt atc att ccc aca gcc cca ctg tat aaa cag att cta			1020
Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu			
305	310	315	320
aat ctg tat gca gag gaa aat gct att gaa gac act atc ttt tac ctt			1068
Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu			
	325	330	335
gga gaa gct ttg cgg cgg gga gtc ata gac ctg gat gtg ttc ctg aaa			1116
Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys			
	340	345	350
cac gtc cgc ctc ctg tcc cgt aaa cag ttc cag cta agg gca cta atg			1164
His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met			
	355	360	365
caa aag gca agg aag act gcg ggc ctt agt gac ctc tac tgacatgtgc			1213
Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr			
	370	375	380
tgtcagctgg agaccgacct ctccgtaaag cattcttttc ttctttctttt tctcatcagt			1273
agaaccacaca ataagttatt gcagttttatc attcaagtgt taaatatttt gaatcaataa			1333
tatatctttct gtttcctttg ggtaaaaact ggctttttatt aatgcacttt ctaccctctg			1393
taagcgtctg tgctgtgctg ggactgactg ggctaaataa aatttggttgc ataaa			1448
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1	5	10	15
Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr			
	20	25	30
Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr			
	35	40	45
Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu			
	50	55	60

Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
 65 70 75 80

Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
 85 90 95

Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser
 100 105 110

Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu
 115 120 125

Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr
 130 135 140

Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser
 145 150 155 160

Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr
 165 170 175

Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser
 180 185 190

Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg
 195 200 205

Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala
 210 215 220

Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala
 225 230 235 240

Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys
 245 250 255

Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val
 260 265 270

Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu
 275 280 285

Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp
 290 295 300

Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu
 305 310 315 320

Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu
 325 330 335

Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys
 340 345 350

His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met
 355 360 365

Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
 370 375 380

<210> 3
 <211> 1494
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 3
 gaaggggtgtg cgattgtgtg ggacgggtctg gggcagccca gcagcgggtg accctctgcc 60
 tgcggggaag ggagtcgcca ggcggccgtc atggcgggtgt cggagagcca gctcaagaaa 120
 atgggtgtcca agtacaaata cagagacctt actgtacgtg aaactgtcaa tggtattact 180
 ctatacaaag atctcaaacc tgttttggat tcatatgttt ttaacgatgg cagttccagg 240
 gaactaatga acctactgg aacaatccct gtgccttata gaggtaatac atacaatatt 300
 ccaatatgcc tatggctact ggacacatac ccatataatc cccctatctg ttttggttaag 360
 cctactagtt caatgactat taaaacagga aagcatgttg atgcaaattg gaagatatat 420
 cttccttata tacatgaatg gaaacacca cagtcagact tgttggggct tattcaggtc 480
 atgattgtgg tatttgagaga tgaacctcca gtcttctctc gtcctatttc ggcacccat 540
 ccgccatacc aggcaacggg gccaccaaact atttcttaca tgccaggcat gccagggtga 600
 atctctccat acccatccgg ataccctccc aatcccagtg gttaccagg ctgtccttac 660
 ccacctggtg gtccatatcc tgccacaaca agttctcagt acccttctca gcctcctgtg 720
 accactgttg gtcccagtag ggatggcaca atcagcgagg acaccatccg agcctctctc 780
 atctctgcgg tcagtgacaa actgagatgg cggatgaagg aggaaatgga tcgtgcccag 840
 gcagagctca atgccttgaa acgaacagaa gaagacctga aaaagggtca ccagaaactg 900

gaagagatgg ttacccgttt agatcaagaa gtagccgagg ttgataaaaa catagaactt 960
 ttgaaaaaga aggatgaaga actcagttct gctctggaaa aaatggaaaa tcagtctgaa 1020
 aacaatgata tcgatgaagt tatcattccc acagctccct tatacaaaca gatcctgaat 1080
 ctgtatgcag aagaaaaacgc tattgaagac actatctttt acttgggaga agccttgaga 1140
 aggggcgtga tagacctgga tgtcttcctg aagcatgtac gtcttctgtc ccgtaaacag 1200
 ttccagctga gggcactaat gcaaaaagca agaaagactg ccggtctcag tgacctctac 1260
 tgacttctct gataccagct ggaggttgag ctcttcttaa agtattcttc tcttcctttt 1320
 atcagtaggt gccagaata agttattgca gtttatcatt caagtgtaaa atattttgaa 1380
 tcaataatat attttctggt ttcttttggt aaagactggc ttttattaat gcactttcta 1440
 tcctctgtaa actttttgtg ctgaatgttg ggactgctaa ataaaatttg tttt 1494

<210> 4
 <211> 390
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 4

Met Ala Val Ser Glu Ser Gln Leu Lys Lys Met Val Ser Lys Tyr Lys
 1 5 10 15

Tyr Arg Asp Leu Thr Val Arg Glu Thr Val Asn Val Ile Thr Leu Tyr
 20 25 30

Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
 35 40 45

Ser Arg Glu Leu Met Asn Leu Thr Gly Thr Ile Pro Val Pro Tyr Arg
 50 55 60

Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
 65 70 75 80

Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
 85 90 95

Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
 100 105 110

Tyr Leu His Glu Trp Lys His Pro Gln Ser Asp Leu Leu Gly Leu Ile

115	120	125
Gln Val Met Ile Val Val Phe Gly Asp Glu Pro Pro Val Phe Ser Arg 130 135 140		
Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn 145 150 155 160		
Thr Ser Tyr Met Pro Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser 165 170 175		
Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro 180 185 190		
Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro 195 200 205		
Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp 210 215 220		
Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp 225 230 235 240		
Arg Met Lys Glu Glu Met Asp Arg Ala Gln Ala Glu Leu Asn Ala Leu 245 250 255		
Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly His Gln Lys Leu Glu Glu 260 265 270		
Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys Asn Ile 275 280 285		
Glu Leu Leu Lys Lys Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu Lys 290 295 300		
Met Glu Asn Gln Ser Glu Asn Asn Asp Ile Asp Glu Val Ile Ile Pro 305 310 315 320		
Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn Leu Tyr Ala Glu Glu Asn 325 330 335		
Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly Glu Ala Leu Arg Arg Gly 340 345 350		
Val Ile Asp Leu Asp Val Phe Leu Lys His Val Arg Leu Leu Ser Arg		

355

360

365

Lys Gln Phe Gln Leu Arg Ala Leu Met Gln Lys Ala Arg Lys Thr Ala
 370 375 380

Gly Leu Ser Asp Leu Tyr
 385 390

<210> 5
 <211> 27
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 5
 aggucaugau ugugguauuu ggagaug

27

<210> 6
 <211> 27
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 6
 caucuccaaa uaccacaauc augaccu

27

<210> 7
 <211> 39
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 7
 caucauac augagguggc uuaugaguau uucuuccag

39

<210> 8
 <211> 39
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 8
 cuacuacuac uacaccuuuu gagcaaguuc agccugguu

39

<210> 9

<211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 9
 ctgataccag ctggaggttg agctcttc 28

<210> 10
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 10
 atttagcagt cccaacattc agcacaaa 28

<210> 11
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 11
 gagaccgacc tctccgtaaa gcattctt 28

<210> 12
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 12
 tagcccagtc agtcccagca cagcacag 28

<210> 13
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 13
 atttagcagt cccaacattc agcacaaa 28

<210> 14

<211> 25
 <212> DNA
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 <220>
 <223> Primer

 <400> 14
 gtcttctctggg tggcagtgat ggcac

25

<210> 15
 <211> 27
 <212> DNA
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 <220>
 <223> Primer

 <400> 15
 cggtgtctcg agagccagct caagaaa

27

<210> 16
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 16
 ccttaccac ctggtggtcc atatcctg

28

<210> 17
 <211> 26
 <212> DNA
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 <220>
 <223> Primer

 <400> 17
 cctccagctg gtatcagaga agtcgt

26

<210> 18
 <211> 27
 <212> DNA
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 <220>
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 <400> 18
 cacagtcaga cttgttgggg cttattc

27

<210> 19

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<400> 19

His Thr His Leu Ala Met Asx Asp Ala
1 5

<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa is any amino acid

<400> 20

Phe Xaa Asn Gly Ala Leu Glx Cys Tyr Ser
1 5 10